

# SEQUENCE LISTING

<110> Rhodes, Kenneth  
An, Wenqian

<120> METHODS FOR TREATING CARDIOVASCULAR DISORDERS

<130> MNI-069CP

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<150> USSN 60/110,277

<151> 1998-11-30

<150> USSN 60/110,033

<151> 1998-11-25

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<151> 1999-07-09

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<170> PatentIn Ver. 2.0

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 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln  
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 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg  
 115 120 125  
 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys  
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- 1997 - 1998
- 1998 - 1999
- 1999 - 2000
- 2000 - 2001

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[illegible]

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Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val	
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Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn Ala Ile Asp Thr Thr  
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 Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu  
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 sequence may be any amino acid

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gtacagaga gaaatgaa ggcagacta ccttcttctt ggcctcag tcaattct 241

tgggttgc aacttacc cctcttgc aatcttga ggccttgc atttctat 301

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 Met Leu Thr Gln

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18

19

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442  
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444  
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454  
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460  
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 461

Cys His Arg Trp Glu Gly Leu Ala Glu Ser Ala Glu Thr Asn Pro

The  $\text{Py}^{\text{H}}$  And  $\text{G}^{\text{H}}$  Are The Val And Tyr And  $\text{Py}^{\text{H}}$  The  $\text{Py}^{\text{H}}$  And  $\text{G}^{\text{H}}$  Are The

Pro Ser Gly Val Val Asn Ala Ala Thr Ile Lys His Ile Tyr Ala His

Pro His Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn  
100 100 110

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val  
115 120 125

The Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys  
188 195 142

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys  
140 150 160

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys  
165 170 175

Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp  
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Val	Phe	Phe	Gln	Lys	Met	Asp	Lys	Asn	Lys	Asp
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(210) 13

< 211 > 2009

(212) DNA

• 213> Homo sapiens

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ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED DATE 01-11-2001 BY 60322 UCBAW

CONFIDENTIAL - SECURITY INFORMATION 100-443886-111-26

SECRET

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798085

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Leu Asp Phe Met Lys Ser Ile Tyr Asn Met Met Gly Lys Tyr Thr Tyr      816

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 222 231

101  
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110 Gln Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu 166  
280 305 330 355 380 405 430 455 480 505 530 555 580 605 630 655 680 705 730 755 780 805 830 855 880 905 930 955 980 1000

4400~ 14  
 Met Arg Gly Ala Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu  
 1 5 10 15  
 Asp Gly Ser Tyr Asp Ala Leu Thr Gly His Pro Ile Gly Pro Thr Lys  
 20 25 30  
 Lys Ala Leu Lys Ala Arg His Leu Lys Leu Leu Pro Cys Cys Gly Pro  
 35 40 45  
 His Ala Leu Ile Ser Val Ser His Thr Leu Ala Ala Pro Ala Ser Leu  
 50 55 60  
 Arg Pro His Arg Pro Arg Leu Leu Asp Pro Asp Ser Val Asp Asp His  
 65 70 75 80  
 Pro Ala Leu Ser Thr Val Cys His Arg Pro Ala Gly Leu Glu Glu Leu  
 85 90 95





$$\begin{aligned} \Delta_{\text{H}}^{\text{H}} &= 1.0 \\ \Delta_{\text{H}}^{\text{H}} &= 2.0 \\ \Delta_{\text{H}}^{\text{H}} &= 1.0 \\ \Delta_{\text{H}}^{\text{H}} &= 2.0 \end{aligned}$$

2400 - 16

Arg	Asp	Leu	Asp	Gly	Ser	Tyr	Asp	Gln	Leu	Thr	Gly	His	Pro	Pro	Gly
1				5					10					15	
Pro	Ser	Lys	Lys	Ala	Leu	Lys	Gln	Arg	Phe	Leu	Lys	Leu	Leu	Pro	Cys
		20					25					30			
Cys	Gly	Pro	Gln	Ala	Leu	Pro	Ser	Val	Ser	Gln	Thr	Leu	Ala	Ala	Pro
		35				40						45			
Ala	Ser	Leu	Arg	Pro	His	Arg	Pro	Arg	Pro	Leu	Asp	Pro	Asp	Ser	Val
	50					55					60				
Glu	Asp	Gln	Ile	Gln	Leu	Ser	Thr	Val	Cys	His	Arg	Pro	Gln	Gly	Leu
65					70					75					80
Glu	Gln	Leu	Gln	Gln	Gln	Thr	Lys	Phe	Thr	Arg	Arg	Gln	Leu	Gln	Val
			85						90						95
Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	Ile	Val	Asn	Glu
		100						105					110		
Glu	Asn	Phe	Lys	Gln	Ile	Tyr	Ser	Gln	Phe	Phe	Pro	Gln	Gly	Asp	Ser
	115						120					125			
Ser	Asn	Tyr	Ala	Thr	Phe	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Asn	His	Asp
	130					135						140			
Gly	Ser	Val	Ser	Phe	Gln	Asp	Phe	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu
145					150					155					160
Arg	Gly	Thr	Ile	Asp	Asp	Arg	Leu	Ser	Trp	Ala	Phe	Asn	Leu	Tyr	Asp
				165					170					175	
Leu	Asn	Lys	Arg	Gly	Cys	Ile	Thr	Lys	Ser	Gln	Met	Leu	Asp	Ile	Met
	180							185					190		
Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Ala	Leu	Ala
	195						200					205			
Gln	Gln	Ala	Phe	Arg	Gln	His	Val	Gln	Ser	Phe	Phe	Gln	Lys	Met	Arg
	210					215						220			
Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Gln	Trp	Ile	Ile	Ala	Ser	Cys
	225				230					235					240
Gln	Gln	Arg	Phe	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu	Phe	Asp	Asn	Val
		245							250					255	

112

&lt;210&gt; 17

&lt;211&gt; 2343

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (131)..(990)

&lt;400&gt; 17

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cgggactctg aggtgggccc taaaatccag cgtcccccag agaaaaagcct tgcagacccc 60
taactccggc cccagacccc agcaggctgc tgcgcgcgca ggggggactg tgtgagcgcc 120
ctatccctggc caccgggggc ccctcccccac ggcccaggcc ggagcggggg gccggggggc 180

atg cgg ggc caa ggt cga aag gag agt ttg tcc gaa tcc cga gat ttg    228
Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
   1             5             10             15

gac ggc tcc tat gac cag ctt acg ggc cac cct cca ggg ccc agt aaa    276
Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
          20             25             30

aaa gcc ctg aag cag cgt ttc ctc aag ctg cta ccg tgc tgc ggg ccc    324
Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
          35             40             45

caa gcc ctg ccc tca gtc agt gaa aca tta gct gcc cca gcc tcc ctc    372
Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
          50             55             60

cgc ccc cac aga ccc cgc ccg ctg gac cca gac agc gtg gag gat gag    420
Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
          65             70             75             80

ttt gaa cta tcc aag gtg tgc cac cgg cct gag ggt ctg gaa caa ctc    468
Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu
          85             90             95

cag gaa caa acc aag ttc aca cgc aga gag ttg cag gtc ctg tac aga    516
Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
          100             105             110

ggc ttc aag aac gaa ttt tcc agc gga att gtc aac gag gaa aac ttc    564
Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
          115             120             125

aag caa att tat tct cag ttc ttt ccc caa gga tat tct agt aac tac    612
Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr
          130             135             140

att att ttt ctc ttc aat ttc ttt gaa aat att tat gat gtt ttt att    660
Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
          145             150             155             160

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1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

2. Next, it is important to gather relevant information and data. This can be done through research, consultation with experts, or by analyzing existing data sets.

3. Once the information is gathered, the next step is to analyze it. This involves identifying patterns, trends, and relationships that can help in understanding the problem.

4. After analysis, the next step is to develop a solution or plan. This involves brainstorming ideas, evaluating options, and selecting the most appropriate approach.

5. Finally, the solution is implemented and the results are evaluated. This involves monitoring the progress, making adjustments as needed, and assessing the overall effectiveness of the solution.

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 2. 1990年2月  
 3. 1990年3月  
 4. 1990年4月

Asp Gly Ser Tyr Asp Glu Leu Thr Gly His Pro Pro Gly Pro Ser Lys  
20 25 30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro  
 35 40 45

Gln Ala Leu Pro Ser Val Ser Gln Thr Leu Ala Ala Pro Ala Ser Leu  
59 15 67

Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Gln Asp Gln  
65 70 75

Thr Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Glu Leu  
 25 50 75

Gln Gln Gln Thr Lys Phe Thr Arg Arg Gln Asp Ser Val Ser Tyr Arg  
132 133 134

Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe  
 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114

Leu Phe Ile Tyr Ser Ala Ile Phe Pro Glu Gly Asp Ser Ser Asn Tyr  
135 145 155

Der	Für	Glt.	Ast		Eur	Vat	All	Rly	Don	Ser	Vat	St-	Don	Anz		Hly	The
1897					1897					1897						1897	

110: Asp Asp Ala Leu Asp Tyr Ala 110: Asp Leu Tyr Asp Leu Ala Tyr

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Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash  
Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash Ash

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Met	Arg	Gly	Gln	Gly	Arg	Lys	Glu	Ser	Leu	Ser	Asp	Ser	Arg	Asp	Leu
1				5					10					15	
Asp	Gly	Ser	Tyr	Asp	Gln	Leu	Thr	Gly	His	Pro	Pro	Gly	Pro	Thr	Lys
			20					25					30		
Lys	Ala	Leu	Lys	Gln	Arg	Phe	Leu	Lys	Leu	Leu	Pro	Cys	Cys	Gly	Pro
		35					40					45			
Gln	Ala	Leu	Pro	Ser	Val	Ser	Glu	Asn	Ser	Val	Asp	Asp	Glu	Phe	Glu
	50					55					60				
Leu	Ser	Thr	Val	Cys	His	Arg	Pro	Glu	Gly	Leu	Glu	Gln	Leu	Gln	Glu
65					70					75					80
Gln	Thr	Lys	Phe	Thr	Arg	Lys	Glu	Leu	Gln	Val	Leu	Tyr	Arg	Gly	Phe
				85					90					95	
Lys	Asn	Glu	Cys	Pro	Ser	Gly	Ile	Val	Asn	Glu	Glu	Asn	Phe	Lys	Gln
			100					105					110		
Ile	Tyr	Ser	Gln	Phe	Phe	Pro	Gln	Gly	Asp	Ser	Ser	Thr	Tyr	Ala	Thr
		115					120					125			
Phe	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Asn	His	Asp	Gly	Ser	Val	Ser	Phe
	130					135					140				
Glu	Asp	Phe	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu	Arg	Gly	Thr	Val	Asp
145					150					155					160
Asp	Arg	Leu	Asn	Trp	Ala	Phe	Asn	Leu	Tyr	Asp	Leu	Asn	Lys	Asp	Gly
				165					170					175	
Cys	Ile	Thr	Lys	Glu	Glu	Met	Leu	Asp	Ile	Met	Lys	Ser	Ile	Tyr	Asp
			180					185					190		
Met	Met	Gly	Lys	Tyr	Thr	Tyr	Ile	Ala	Leu	Arg	Glu	Glu	Ala	Pro	Arg
		195					200					205			
Glu	His	Val	Gln	Ser	Phe	Phe	Gln	Lys	Met	Asp	Arg	Asn	Lys	Asp	Gly
	210					215					220				
Val	Val	Thr	Ile	Glu	Glu	Phe	Ile	Glu	Ser	Cys	Gln	Lys	Asp	Glu	Asn
225					230					235					240

[illegible]

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- 22.0 •
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8490 - 21	
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cgttgagcacj aaajggggag ctgtgtgagcc gccctattct ggccacccccjg agccaccttc	180
caaggccccag gaggttandg gggccggggg grc att tgg ggr caa agr aga aag	234
	Met Arg Gly Gln Gly Arg Lys
	1 5
gag agt ttg tcc gaa tcc cga gat ctg gac ggc tcc tat gac cag ctt	282
Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu	
10 15 20	
aag ggc cac ccg taa ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc	330
Thr Gly His Pro Pro Gly Pro Ser Lys Iys Ala Leu Lys Gln Arg Phe	
25 30 35	
ctc aag ctg ctg ccg tgc tgc ggg ccc caa ggc ctg cac tca gtc agt	378
Leu Lys Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser	
40 45 50 55	
gaa aac agc gta gag gat gag ttt gaa tta tcc acy gig tgt cac cga	426
Glu Asn Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg	
60 65 70	
cct gag ggc ctg gaa caa ctc cag gaa cag acc aag ttc aca ccg aga	474
Pro Glu Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg	
75 80 85	
gag ctg cag gtc ctg tac cga ggc ttc aag aac gta tgc ccc agt ggg	522
Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly	
90 95 100	
att ctc aac gag gag aac ttc aag caa att tat ttt cag ttt ttt cag	570
Ile Val Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro	
105 110 115	
caa gga gar ttc agc aac tat gtc act ttt ctc ttc att gac ttt gar	618
Gln Gly Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp	
120 125 130 135	
agt aat caa tat ggt ctt ctc att ttt gag gar ttc gtc gtt agt ttg	666
Thr Asn His Asp Gly Ser Val Ser Phe Gln Asp Phe Val Ala Gly Leu	
140 145 150	



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&lt;210&gt; 20

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Rattus sp.

&lt;400&gt; 22

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu  
 1 5 10 15

Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys  
 20 25 30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro  
 35 40 45

Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu  
 50 55 60

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu  
 65 70 75 80

Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe  
 85 90 95

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln  
 100 105 110

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr  
 115 120 125

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe  
 130 135 140

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp  
 145 150 155 160

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly  
 165 170 175

Cys Ile Thr Lys Gln Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp  
 175 180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Gln Gln Ala Pro Arg  
 195 200 205

Gln His Val Gln Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly  
 210 215 220

Val Val Thr Ile Ala Glu Ile Ile Ala Ser Cys Glu Ala Arg Ala Asn  
 235 240 245

Ile Met Arg Ser Met Glu Leu Ile Arg Ser Val Leu  
 245 250

<123> 23  
 <121> 1-59  
 <122> 10A  
 <113> Homo sapiens

<123>  
 <121> CDS  
 <122> (127)..(506)

<100> 23  
 atcaatgat gactgtgtt ccaatctgt ctccaggacc tccgggtaga ctccagacc 60  
 cgggcacatt cccagacta gctgagac ggtcttccc agccacagaa gacacaggg 120  
 cggccagggtt aggtgtgtt aggtcttat cgggcacac cgggcacac tccacaggac 180  
 cgggcagggtt cgggtgggtt ggggac atg cgg ggc cag ggc cgc aac gag agt 233  
 Met Arg Gly Gln Gly Arg Lys Glu Ser  
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ttg tcc gat tcc cga gac atg gag ggt tcc tcc gac cag ctg acg gac 281  
 Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Asp  
 10 15 20 25

agc gtg gac gat gaa ttt gaa ttg tcc acc ggt tgt cag cgt cct gag 329  
 Ser Val Asp Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu  
 30 35 40

ggt ctg gag cag ctg cag gag aac aaa ttc acg cgc aag gag ttg 377  
 Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu  
 45 50 55

cag gtc ctg tcc cgg ggc ttc aag aac gaa tgt ccc agc gaa att gtc 425  
 Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val  
 60 65 70

aat gag gag aat ttc aat cag att tcc tcc cgt ttc ttc aat gaa gaa 473  
 Asn Gln Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly  
 75 80 85

gac tcc agc acc tat ggc aat tat ctg tcc aat ggc att ttc ttc aac 521  
 Asp Ser Ser Thr Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn  
 90 95 100 105

tat gat ggt tcc ttc gat ttt agt gaa ttt atg ggt ggt ttt tcc ttc 569  
 His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val  
 110 115 120

att ttc cgt ggt att tta tat gac aat ttc aat ttt ggt ttc aat ttc 617  
 Ile Leu Arg Gly Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu  
 125 130 135

tat gat gtt aat aat tat gtt ttt ttt ttt aat tat tat aat ttt gtt 740  
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Gln Glu Met Leu Asp  
 14 114 150  
 att aat aat ttt att tat aat ttt ttt ttt gtt ttt ttt aat ttt ttt 741  
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Phe Ala  
 150 160 165  
 ttt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt 761  
 Leu Arg Glu Gln Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys  
 170 175 180 185  
 att gat aat aat aat gat gat gat gat gat gat gat gat gat gat gat 800  
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu  
 190 195 200  
 ttt ttt gaa aag gat gat gat aat att gtt gtt ttt att gat gat gtt ttt gtt 857  
 Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp  
 205 210 215  
 aat gtt aat tttttttttt gttttttttt gttttttttt gttttttttt 900  
 Asn Val Ile  
 220  
 atgtatatac cctagtccag gggacatca cctttcttt cccaggtcta tcttcattct 966  
 aagcctccct gggggtctga gggatcraag agtttgggga tttagtagtc agatctctg 1026  
 gagctgaagg gggcagagag tgggcagagt gcatctgggg ggggtttccc aactcccacc 1086  
 agctctcacc cctttcttg ctgacaccca gtgttgagag tgcctcctct gtaggaattg 1146  
 agcgggtccc cactctctac cctactctag aacacacta gaggatgtc tctgtctatg 1206  
 gtgtttccc cttctctgac ctatataaca tttctctaa gactcctctc ttagagagaa 1266  
 tctctcattc ttggcaattg ctgggtttct agacagcca tttagagccc tgggggaggg 1326  
 ggacaagaat gtataggga aaatcttgg cctgagtcaa tggataggtc ctaggagggt 1386  
 ggtgggttg agaatagaa gggctggaa gatttatatt gctcaggcat aacagttat 1446  
 agctccaaat tctcaggtt tgttctctt gttcttaa atctaatg ctagggttg 1506  
 cagagagct tttctctta gaaatgctc agatatttc caccctctc tgggtatcca 1566  
 tggagagct ggttcagat atttgatca tcttggtt tttctctt cctctctta 1626  
 tctatgtt gtttgggt gttgtggtt ttttgggt gtttgggt ttttgggt 1686  
 ctgacaat tttctctt cttctctt ttttgggt gtttgggt gtttgggt 1746  
 agttctct ttttgggt ttttgggt ttttgggt ttttgggt ttttgggt 1806  
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<211> 124  
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 <211> 126  
 <211> Hima sapiens

<211> 124  
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu  
 1 5 10 15  
 Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Asp Asp Gln Phe Glu  
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 Leu Ser Thr Val Cys His Arg Pro Gln Gly Leu Gln Gln Leu Gln Glu  
 35 40 45  
 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe  
 50 55 60  
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln  
 65 70 75 80  
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr  
 85 90 95  
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe  
 100 105 110  
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp  
 115 120 125  
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly  
 130 135 140  
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp  
 145 150 155 160  
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg  
 165 170 175  
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly  
 180 185 190  
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn  
 195 200 205  
 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile  
 210 215 220

<212> 25  
 <211> 2101  
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 <213> Similar sp.

<220>  
 <221> CDS  
 <222> (123)...(124)  
 <400> 25

[illegible]

[illegible]

- 210 • 26
- 211 • 26
- 212 • 197
- 213 • similar, see

• 475 • 66

Met Arg Gly Gln Gly Arg Lys Gln Ser Leu Ser Asp Ser Arg Asp Leu  
1 5 10 15

Asp Gly Ser Tyr Asp Val Leu Thr Asp Ser Val Glu Arg His Ileu Glu

Leu Ser Thr Val Tyr His Arg Ile Glu Gly Leu Glu Gln Leu His His  
 1 4 45  
 Ala Thr Lys Ile Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Ile  
 55 60  
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Ala Glu Asn Ile Lys Gln  
 65 70 75  
 Ile Tyr Ser Gln Ile Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr  
 85 90 95  
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Ile  
 105 110  
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp  
 115 120 125  
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly  
 130 135 140  
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp  
 145 150 155 160  
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg  
 165 170 175  
 Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly  
 180 185 190  
 Val Val Thr Ile Glu Glu Phe Ile Gln Ser Cys Gln Lys Asp Glu Asn  
 195 200 205  
 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile  
 210 215 220

&lt;210&gt; 27

&lt;211&gt; 2057

&lt;212&gt; DNA

&lt;213&gt; Simian sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (208)...(303)

&lt;400&gt; 27

MTTGGGGA GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG 63

GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG 123

GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG 183

GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG GGTGGG 243

Met Arg Gly Gln Gly Arg Lys Glu Ser

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ttt ttt gaa ttt gaa gat ttt ttt ttt ttt ttt gat gat ttt ttt gaa ttt	471
Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Glu Leu Thr Gly	
1 21 27	
gaa ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	487
His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Glu Arg Phe Leu Lys	
32 38 40	
ctg ctg ctg tgc tgc ggg gaa gaa gaa ctg gaa taa gtc agt gaa aac	507
Leu Leu Pro Cys Cys Gly Pro Glu Ala Leu Pro Ser Val Ser Glu Asn	
43 47 55	
agt gaa gaa gat gat gag ttt gaa tta ttt arg ctg ttt gaa gaa gaa gag	426
Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu	
60 65 70	
ggc ctg gaa gaa ctg caa gaa gaa gaa ctg gaa taa gaa gaa gag ctg	474
Gly Leu Glu Glu Leu Glu Glu Glu Thr Lys Phe Thr Arg Arg Glu Leu	
75 80 85	
gag gtc ctg ttc gaa ggc ttt aag aac gaa tgc gaa agt ggg att gtc	522
Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val	
90 95 100 105	
aac gag gag aac ttc aag caa att tat tct cag ttc ttt ccc caa gga	570
Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly	
110 115 120	
gaa ttc aga aac tat ggt act ttt ctg ttc aat ggt ttt gaa acc aac	618
Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn	
125 130 135	
caa gat ggc tct gtc agt ttt gag gac ttt gtc ggt ggt ttg tgg gtc	666
His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val	
140 145 150	
att ctt cgg ggg acc ata gat gat aga ctg agc tgg ggt ttc aac tta	714
Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu	
155 160 165	
tat gac ctg aac aag gaa ggc tgt atc aca aag gag gaa atg ctt gac	762
Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp	
170 175 180 185	
att atg aag ttc atc tat gaa atg atg ggc aag ttc aac tat ggt gaa	810
Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala	
190 195 200	
ctc cgg gag gag gaa gaa gaa gaa gaa ggc gag agc ttc ttc cag aag	858
Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Glu Lys	
205 210 215	
atg gac atg atc aac tat ggt ttc ctg aat atc gaa gaa ttc atc gaa	906
Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu	
220 225 230	
tat ttt gaa ttt gaa gaa gaa atc atg aag ttc atc gaa ttc tta gaa	954
Ser Cys Glu Glu Asp Glu Asn Ile Met Arg Ser Met Glu Leu Ser Pro	
235 240 245	

[illegible]

- 210 : 25
- 211 : 250
- 212 : FRT
- 213 : SIM140 98

1400 - 2-

Met Arg Gly Gln Gly Arg Lys Gln Ser Leu Ser Glu Ser Arg Asp Leu  
1 6 10 15

Asp Gly Ser Tyr Asp Phe Leu Thr Gly His Pro Phe Gly Pro Ser Lys  
20 25 30

Lys Ala Leu Lys Gln Arg His Leu Lys Leu Leu Pro Cys Cys Gly Pro  
35 40 45

Gln Ala Leu Pro Ser Val Ser Gln Asn Ser Val Glu Asp Glu Phe Glu  
50 55 60

Leu Ser Thr Val Tyr His Arg Pro Gln Gly Leu Glu Glu Leu Glu Glu  
65 70 75 80 85

Val Thr Tyr Ile Thr Arg Arg Val Leu Ala Val Leu Tyr Arg Gly Ile  
 100  
 Lys Asn Ala Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Ile Lys Phe  
 110  
 Ile Tyr Ser Ala Phe Phe Pro Ala Gly Asp Ser Ser Asn Tyr Ala Thr  
 120  
 Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe  
 130  
 Glu Asp Ile Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp  
 140  
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly  
 150  
 Cys Ile Thr Lys Gln Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp  
 160  
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg  
 170  
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly  
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 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn  
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 Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn  
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<210> 29  
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 <212> DNA  
 <213> Rattus sp.

<220>  
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 <222> (111..1404)

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 1 5 10 15  
 cga tat cct tac cag tgg gta att ggg tgg tgg ttg gaa gaa ggc gta 96  
 Arg Ser Leu Tyr Gln Leu Val Thr Val Cys Ser Leu Ser Pro Asp Ser Val  
 20 25 30 35  
 tgg gat tgg ttg gaa tta taa aac cta tgg taa tta ctt tgg ggt gta 144  
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu  
 40 45 50  
 tta gaa cct tgg gaa cct att att tta aca ttt aac ggt tta ggt ttt 180  
 Ala Glu Leu Val Glu Val Val Lys Phe Thr Arg Arg Glu Leu Glu Val  
 55 60

147  
 Lys Tyr Arg Gly Ile Lys Asn Ile Tyr Ile Ser Gly Ile Val Asn Glu  
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151  
 Glu Asn Phe Lys Glu Ile Tyr Ser Gln Ile Phe Pro Gln Gly Asp Ser  
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155  
 Ser Asn Tyr Ala Thr Phe Leu Ile Asn Ala Ile Asp Thr Asn His Asp  
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159  
 Gly Ser Val Ser Ile Glu Asp Ile Val Ala Gly Leu Ser Val Ile Leu  
 162

163  
 Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp  
 166

167  
 Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met  
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171  
 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg  
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175  
 Gly Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp  
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179  
 Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys  
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183  
 Gln Glu Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val  
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[illegible]

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<211> 225  
<212> PRT  
<213> Rattus sp.

4400> 30

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Arg	Ser	Leu	Tyr	Gln	Leu	Val	Thr	Gly	Ser	Leu	Ser	Pro	Asp	Ser	Val
		20						25					30		
Glu	Asp	Gln	Phe	Gln	Leu	Ser	Thr	Val	Cys	His	Arg	Pro	Gln	Gly	Leu
		35					40						45		
Gln	Gln	Leu	Gln	Gln	Gln	Thr	Lys	Phe	Thr	Arg	Arg	Glu	Leu	Gln	Val
		50				55						60			
Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Gln	Cys	Pro	Ser	Gly	Ile	Val	Asn	Gln
	65				70					75					80
Glu	Asn	Phe	Lys	Gln	Ile	Tyr	Ser	Gln	Phe	Phe	Ile	Gln	Gly	Asp	Ser
			85						90					95	
Ser	Asn	Tyr	Ala	Thr	Ile	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Asn	His	Asp
		100						105					110		
Gly	Ser	Val	Ser	Phe	Gln	Asp	Ile	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu
		115					120					125			
Arg	Gly	Thr	Ile	Asp	Asp	Arg	Leu	Ser	Trp	Ala	Ile	Asn	Leu	Tyr	Asp
	130					135					140				
Leu	Asn	Lys	Asp	Gly	Tyr	Ile	Thr	Lys	Gln	Gln	Met	Leu	Asp	Ile	Met
145					150					155					160

Thr Tyr Ala His Phe Leu Ile Asn Ala Ile Asp Ala Asp Gly Asn Gly 44

430 aac cag ttt gaa gag ttt gta gtt ttt cta ttt atc atg ttt ggt 440  
 Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg  
 145 155 165

450 aac gta gaa gag gag cta gag ttt gaa ttt aat cta taa gag att 460  
 Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile  
 165 170 175

470 aac aag gat ggt tac atc acc aac gag gag atg atg gac atc atg aag 480  
 Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys  
 180 185 190

490 tcc atc tat gac atg atg ggc cgc cgc acc tac ccc atc atg cgg gag 500  
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu  
 195 200 205

510 gac gag cgg gag gag cag gta gag agg ttc ttc gag aaa atg gac cgg 520  
 Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg  
 210 215 220

530 aac cag gat ggg gta gta acc att gaa gag ttc atg gag gac tgt cag 540  
 Asn Glu Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Glu  
 225 230 235 240

550 aag gat gag aac atc atg agc tcc atg cag atg ttt gag aat gtc atc 560  
 Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile  
 245 250 255

taggacacgt ccaaaggagt gcattggcac agccacctcc accccaaga aacctccatc 828  
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 gotacacaca cacacacaca cacacacaca cacacacaca cacagccatt catctgggct 948  
 ggcagagggg acagagttca gggaggggct gagctctggct aggggcagag tccaggagcc 1008  
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&lt;211&gt; 256

&lt;212&gt; 187

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

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Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Gln Gly Ile Lys Trp  
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Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val  
 35 40 45

Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp  
 50 55 60

Ser Gln Leu Glu Leu Ser Thr Val Arg His Gln Thr Gln Gly Leu Asp  
 65 70 75 80

Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu  
 81 87 93

Tyr Arg Gly Phe Lys Asn Gln Cys Ile Thr Gly Ile Val Arg Phe Arg  
 100 106 112

Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr  
 115 120 125

Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly  
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Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg  
 145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile  
 165 170 175

Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys  
 180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu  
 195 200 205

Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg  
 210 215 220

Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln  
 225 230 235 240

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile  
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 1 5 10 15

cat gag aag ctc aag tgg gcc ttc aat ctc tac gac atc aac aag gac 96  
 His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp  
 20 25 30

ggt tac atc aac aaa cag gag atg ctg ggc atc atg aat ttt atc tac 144  
 Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr  
 35 40 45

ggt atg atg ggt ggt cag aac ttt ctt ata ggt ggt gag ggt ggt ggt 192  
 Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Gln Asp Ala Pro  
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 ggc ggt ttc ctg tac gct cag aac agc acc aag cgc agc att aaa gag 96  
 Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu  
 20 25 30  
 cgg ctg atg aag ctg ttg ccc tgc tca gct gcc aaa acg tgg tct cct 144  
 Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro  
 35 40 45  
 gct att caa aac agc ggc gaa gat gaa ctg gag atg gcc acc gtc agg 192  
 Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg  
 50 55 60  
 cat cgg ccc gaa gcc ctt gag ctt ctg gaa gcc cag agc aaa ttt acc 240  
 His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr  
 65 70 75 80  
 aag aaa gag ctt cag atc ctt tac aga gga ttt aag aac gta aga act 288  
 Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr  
 85 90 95  
 ttc ttt ttg act tta cct tca cac aat tcc cag agg agc att gag aaa 336  
 Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys  
 100 105 110  
 tggagagaaa agggggaaaa tatcccatto tatgagaagc cccatccatat gtatatttca 396  
 tactgatcct tcccagatag gaataaato agtatctgtg gaatttgaat ctctgtggca 456  
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 <213> Homo sapiens

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Arg Leu Met Lys Leu Leu His Lys Ser Ala Ala Lys Thr Ser Ser Pro  
4 4

Ala Ile Val Asn Ser Val His Asp Glu Leu His Met Ala Thr Val Arg  
1 1 1

His Arg Leu His Ala Leu His Leu Leu Glu Ala Glu Ser Lys His Thr  
65 70 75 80

Lys Lys Glu Leu Glu Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr  
85 90 95 100

Phe Phe Leu Thr Leu Pro Ser His Asn Ser Glu Arg Ser Ile His Lys  
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<213> Homo sapiens

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<221> CDS

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att gaa gag ttc ctg gag aac tgt cag aag gat gag aac atc atg acc 97  
Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser  
20 25 30

tcc atg ccc ctg ttc gag aat gtc atc tgggacgtt ccacagggtt 144  
Ser Met Gln Leu Phe Glu Asn Val Ile  
35 40

gcattggcgc accactcgc accacacaga aactcgcgc atgcacaggag cagactccaa 204

gaaactctc accatagat ttcccaaaag tgaacattt gctacacac cctacacac 264

cacacacac cctacacac cctacacatt cacttggtt ggcagagttt accatttcc 324

gagaggttt accctggtt accctgagc tccattttt cctagcagcc ctcacaggtt 384

caggagttt accctgctc ttttgatg gttttttt caggtctt gttttttt 444

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gcctccctt cctacacac cctacacac cctacacac cctacacac cctacacac 624

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<213> Homo sapiens

<214> 40

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26

26

30

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<213> Rattus sp.

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ggtggcagg ggtctgtgt ggtggccc tttggccc ggtggccc gtttgggc 180  
ccaggcgggt ggtggccc ggtggccc atg tgg ggc caa ggc aga aag gtt agt 234  
Met Arg Gly Gln Gly Arg Lys Gln Ser  
1 5

tgg tgg gaa tgg cga gat ctg gac ggc tgg tat gac cag ctt aat ggc 282  
Leu Ser Gln Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly  
10 15 20 25

cac cct cca tgg ccc agt aaa aaa ggc ctg aag cag cgt ttc cca aag 330  
His Pro Irs Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys  
30 35 40

ctg ctg cag tgg tgc ggg ccc caa ggc ctg ccc taa gtc agt gaa aac 378  
Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Gln Asn  
45 50 55

agg gaa gag gat gag ttt gaa tta tta arg gtt ttt cca cga ctt gag 426  
Ser Val Gln Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu  
60 65 70

agg ctt gaa gaa ctt cag gaa ctt aat ttt tta aat ctt agt gaa ctg 474  
Gly Leu Gln Gln Leu Gln Gln Gln Thr Lys Phe Thr Ala Arg Gln Leu  
75 80 85

cag gaa ctt taa cga ggc ttt aag aat tta ttt ctt ctt gtt aat gtc 522  
Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val  
90 95 100 105

aac gaa gaa aat ctt aat aat aat ttt ttt ctt ttt ttt ctt aat aat 570  
Asn Gln Gln Asn Phe Lys Gln Ile Tyr Ser Gln Phe Ile Pro Gln Gly  
110 115 120

gaa ttt aat aat ttt aat aat ttt ttt aat gtt ttt gaa aat aat 618  
Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn  
125 130 135

aac ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 666  
His Asp Gly Ser Val Ser Phe Gln Arg Phe Val Ala Gly Leu Ser Val  
140 145 150

[illegible]

Protein Data Bank (PDB) accession number: 1A23

Protein name: Bacterial ribonuclease H1

413-42  
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411-42

413-42

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Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys  
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Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro  
35 40 45

Gln Ala Leu Pro Ser Val Ser Gln Asn Ser Val Glu Asp Gln Phe Gln  
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Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Gln  
65 70 75 80

Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe  
85 90 95

Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln  
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Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr  
115 120 125

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe  
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Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp  
145 150 155 160

Asp Arg Leu Ser Thr Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly  
165 170 175

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp  
180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg  
195 200 205

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly  
210 215 220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Glu Gln Asp Glu Asn  
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Ile Met Arg Ser Met Gln Leu Ser Leu Leu Asn  
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<111> 40

<112> DNA

<113> Rattus sp.

<120>

<121> Xaa at positions 2,5,6,8,11,15 and 20 may be Ile, Leu, Val or Met

<122>

<123> Xaa at positions 3,4,7,8,10,15-20,23 and 24 may be any amino acid

<130>

<131> Description of Artificial Sequence: consensus motif

<400> 43

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Asp Gly Asp Gly Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Glu Phe Xaa Xaa Xaa Xaa  
20 25

<210> 44

<211> 40

<212> DNA

<213> Rattus sp.

<410> 44

taataagact caataatagg agtaggcata atgtatcag 40

<210> 45

<211> 40

<212> DNA

<213> Rattus sp.

<400> 45

attacacata actaaaggga caatactgtt taagctcaa 40

<210> 46

<211> 40

<212> DNA

<213> Rattus sp.

<410> 46

taataagact caataatagg agtaggcata atgtatcag 40

<210> 47

<211> 40

<212> DNA

<213> Rattus sp.

<410> 47

attacacata actaaaggga caatactgtt taagctcaa 40



Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys



Met Leu Thr Leu Glu Trp Glu Ser Glu Gly Leu Gln Thr Val Gly Ile  
 1 5 10 15  
 Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu  
 20 25 30  
 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr  
 35 40 45  
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys  
 50 55 60  
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu  
 65 70 75 80  
 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser  
 85 90 95  
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe  
 100 105 110  
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe  
 115 120 125  
 Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu  
 130 135 140  
 Asn Trp Ala Ile Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr  
 145 150 155 160  
 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly  
 165 170 175  
 Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val  
 180 185 190  
 Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr  
 195 200 205  
 Ile Asp Glu Ile Ile Glu Ser Cys His Lys Asp Glu Asn Ile Met Arg  
 210 215 220  
 Ser Met Gln Leu Phe Glu Asn Val Ile  
 225 230

<210> 49  
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 20 25 30  
 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr  
 35 40 45  
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys  
 50 55 60  
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu  
 65 70 75 80  
 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser  
 85 90 95  
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe  
 100 105 110  
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe  
 115 120 125  
 Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu  
 130 135 140  
 Asn Trp Ala Ile Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr  
 145 150 155 160  
 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly  
 165 170 175  
 Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val  
 180 185 190  
 Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr  
 195 200 205  
 Ile Asp Glu Ile Ile Glu Ser Cys His Lys Asp Glu Asn Ile Met Arg  
 210 215 220  
 Ser Met Gln Leu Phe Glu Asn Val Ile  
 225 230

Val Asn Ile Val Thr Val Glu Ala Gly Pro Val Arg Ser His Met  
Gly Thr Val Val Glu Lys Leu Asp Trp Ala Phe Asn Leu Tyr Asp Ile

11                      111                      111

[illegible]

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Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Gln Ala Gln Ser Lys  
 55 65 75  
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Gln  
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 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser  
 110 120 130  
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe  
 135 145 155  
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe  
 160 170 180  
 Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu  
 185 195 205  
 Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr  
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 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly  
 235 245 255  
 Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val  
 260 270 280  
 Glu Thr Phe Phe Gln Ala Val Phe His Cys Ile Ile Lys Trp Lys Phe  
 285 295 305  
 Lys Thr Ala Ser Asn Lys Thr Arg Met Phe Thr Asp Ile Cys Lys Gly  
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 Ser Gly Tyr Leu Ser Ser Ser Ile Cys  
 335 345

&lt;210&gt; 52

&lt;211&gt; 2051

&lt;212&gt; DNA

&lt;213&gt; Rattus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (85)..(1305)

&lt;400&gt; 52

ggtaggagcta agcaatcaat ggggtgctga cctgggtctg cagataaaaa ggaagagcttc 60

tctgagggg tctcagctga caaa atg aac ggc gtg gaa ggt aac aac gag 111

Met Asn Gly Val Glu Gly Asn Asn Glu

1

5

ctc cct ctc ggt aac acc tag acc tac gcc ctt gtc cag gaa gat ctg 159

Leu Pro Leu Ala Asn Thr Ser Thr Ser Ala Leu Val Pro Glu Asp Leu

10

15

20

25

tat atg aag cag tat cag tggcttc agt gag gaa act gac atg gta ggt 237

Asp Leu Lys Gln Asp Gln Pro Leu Ser Glu Glu Thr Asp Thr Val Arg

30

35

40

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Glu Met Glu Ala Ala Gly Glu Ala Gly Ala Glu Gly Gly Ala Ser Pro	
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gat ttc gaa gaa ttc gac gaa gag atg ttc gtc gaa atg gaa gat gat	336
Asp Ser Glu His Cys Asp Pro Gln Leu Cys Leu Arg Val Ala Glu Asn	
60 65 70	
ggc tgt ggt ggc gaa ggc gga gag ggg ctg gag gat ggt atg ttc tca	351
Gly Cys Ala Ala Ala Ala Gly Glu Gly Leu Glu Asp Gly Leu Ser Ser	
75 80 85	
tca aag tgt ggg gaa gaa ccc ttc ggc tct gtc gaa gcc aac gac agc	399
Ser Lys Cys Gly Asp Ala Pro Leu Ala Ser Val Ala Ala Asn Asp Ser	
90 95 100 105	
aat aaa aat ggc tgt cag ctt gaa ggc cag ctg agc cct gct aag cca	447
Asn Lys Asn Gly Cys Gln Leu Ala Gly Pro Leu Ser Pro Ala Lys Pro	
110 115 120	
aaa act ctg gaa gcc agt ggt gaa gtg ggc ctg ggg tgc cag atg atg	495
Lys Thr Leu Glu Ala Ser Gly Ala Val Gly Leu Gly Ser Gln Met Met	
125 130 135	
cca ggg ccg aag aag acc aag gta atg act acc aag ggc gcc atc tct	543
Pro Gly Pro Lys Lys Thr Lys Val Met Thr Thr Lys Gly Ala Ile Ser	
140 145 150	
ggc act aca ggc aag gaa gga gaa gca ggc ggc gca atg cag gaa aag	591
Ala Thr Thr Gly Lys Glu Gly Glu Ala Gly Ala Ala Met Gln Glu Lys	
155 160 165	
aag ggg gtg cag aaa gaa aaa aag gca gct gga gga ggg aaa gac gag	639
Lys Gly Val Gln Lys Glu Lys Lys Ala Ala Gly Gly Gly Lys Asp Glu	
170 175 180 185	
act cgt cct aga gcc cct aag atc aat aac tgc atg gac tcc ctg gaa	687
Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu	
190 195 200	
ccc atc gat caa gag ctg tca aat gta aat gag caa gct gac agg gcc	735
Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala	
205 210 215	
ttc ctg cag ctg gaa cgc aaa ttt ggg cgg atg aga agg ctg cag atg	783
Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met	
220 225 230	
cag cgc cga agt ttc atc atc caa aac atc caa ggt ttc tgg gta acg	831
Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr	
235 240 245	
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Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp	
250 255 260 265	
tta gac atg atg agt ttc atc atc aat tta gag gaa gag gag ttc aag	927
Glu Asp Met Met Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys	
270 275 280	

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000



4110-13

4110-407

4110-187

4110-187

4110-13

Met Asn Gly Val Glu Gly Asn Asn Glu Leu Pro Leu Ala Asn Thr Ser  
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Thr Ser Ala Leu Val Pro Glu Asp Leu Asp Leu Lys Gln Asp Gln Pro  
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Leu Ser Glu Glu Thr Asp Thr Val Arg Glu Met Glu Ala Ala Gly Glu  
35 40 45

Ala Gly Ala Glu Gly Gly Ala Ser Pro Asp Ser Glu His Cys Asp Pro  
50 55 60

Gln Leu Cys Leu Arg Val Ala Glu Asn Gly Cys Ala Ala Ala Ala Gly  
65 70 75 80

Glu Gly Leu Glu Asp Gly Leu Ser Ser Ser Lys Cys Gly Asp Ala Pro  
85 90 95

Leu Ala Ser Val Ala Ala Asn Asp Ser Asn Lys Asn Gly Cys Gln Leu  
100 105 110

Ala Gly Pro Leu Ser Pro Ala Lys Pro Lys Thr Leu Glu Ala Ser Gly  
115 120 125

Ala Val Gly Leu Gly Ser Gln Met Met Pro Gly Pro Lys Lys Thr Lys  
130 135 140

Val Met Thr Thr Lys Gly Ala Ile Ser Ala Thr Thr Gly Lys Glu Gly  
145 150 155 160

Glu Ala Gly Ala Ala Met Gln Glu Lys Lys Gly Val Gln Lys Glu Lys  
165 170 175

Lys Ala Ala Gly Gly Gly Lys Asp Glu Thr Arg Pro Arg Ala Pro Lys  
180 185 190

Ile Asn Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser  
195 200 205

Asn Val Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys  
210 215 220

Phe Gly Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile  
225 230 235 240

Gln Asn Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln  
245 250 255

Leu Ser Pro Met Ile Ser Gly Gln Asp Glu Asp Met Met Arg Tyr Met  
260 265 270

Ile Asn Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys  
275 280 285

His Lys His Leu His Ala Ser Asn Ile Tyr His Arg Asn Val Gly Leu  
 24 28 32  
 Val Lys Ala Tyr His Arg Asn Ser Asn Gly Arg Val Val Ser Leu Ser  
 36 40 44 48 52  
 Thr Pro Ile Arg Tyr His Arg Gly Ala Glu Ile Ala Ala His Ile His  
 56 60 64 68 72  
 Arg Asn Arg Glu Gly Asn Thr Ile Pro Ser His Ile Asn Thr Ile Ser  
 76 80 84 88 92  
 Asp His Ser Leu Leu Val Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly  
 96 100 104 108 112  
 Glu Leu Trp Ser Asn Pro Leu Glu Tyr Tyr Leu Met Gly Asp Gly Pro  
 116 120 124 128 132  
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 136 140 144 148 152  
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&lt;210&gt; 54

&lt;211&gt; 4148

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54)..(1329)

&lt;400&gt; 54

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 Met Ser Gly Leu Asp Gly Gly Asn Lys  
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ttc act ctg ggc caa att ggc att ctg gat att cca gac atc aac cca 162  
 Leu Pro Leu Ala Gln Thr Gly Gly Leu Ala Ala Pro Asp His Ala Ser  
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 Gly Asp Pro Asp Leu Asp Gln Cys Gln Gly Leu Arg Gln Glu Thr Glu  
 30 35 40

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 Ala Thr Glu Val Met Ala Asn Thr Gly Gly Gly Ser Leu Val Thr Val  
 45 50 55

att gat att att gga ttt cca att att ctg atg ttt att att att att 306  
 Ala Glu Gly Gly Ala Ser Glu Asp Pro Val Asp Cys Gly Pro Ala Leu  
 60 65 70

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cag tgg gat gtt cca ctt tat atg aaa gtt cta gaa cca gat ttt ttc Gln Glu Asp Ala Pro Pro Ser Thr Lys Gly Leu Glu Ala Ala Ser Ala 90 95 100 105	402
gac gag gct gct gat agt agt cag aaa aat ggc tgt cag ctt gga gag Ala Glu Ala Ala Asp Ser Ser Gln Lys Asn Gly Cys Gln Leu Gly Glu 110 115 120	452
ccc cgt gga cct gct ggg cag aag ggt cta gaa gcc tgt ggc gca ggg Pro Arg Gly Pro Ala Gly Gln Lys Ala Leu Glu Ala Cys Gly Ala Gly 125 130 135	498
ggc ttg ggg tat cag atg ata ccc ggg aag aag gcc aag gaa gtg aag Gly Leu Gly Ser Gln Met Ile Pro Gly Lys Lys Ala Lys Glu Val Thr 140 145 150	546
act aaa aaa cgc gcc atc tcg gca gca gtg gaa aag gag gga gaa gca Thr Lys Lys Arg Ala Ile Ser Ala Ala Val Glu Lys Glu Gly Glu Ala 155 160 165	594
ggg gcg gcg atg gag gaa aag aag gta gtg cag aag gaa aaa aag gtg Gly Ala Ala Met Glu Glu Lys Lys Val Val Gln Lys Glu Lys Lys Val 170 175 180 185	642
gca gga ggg gtg aaa gag gag aca cgg ccc agg gcc ccg aag atc aat Ala Gly Gly Val Lys Glu Glu Thr Arg Pro Arg Ala Pro Lys Ile Asn 190 195 200	690
aac tgc atg gac tca ctg gag gcc atc gat caa gag ttg tca aac gta Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser Asn Val 205 210 215	738
aat gcc cag gct gac agg gcc ttc ctt cag ctt gag cgc aag ttt ggc Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys Phe Gly 220 225 230	786
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atc cca ggt ttc tgg gtt act gcc ttt cga aac cac ccc cag ctg tca Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln Leu Ser 250 255 260 265	882
cct atg atc agt ggc caa gat gaa gac atg ctg agg tac atg atc aat Pro Met Ile Ser Gly Gln Asp Glu Asp Met Leu Arg Tyr Met Ile Asn 270 275 280	930
ttg gag gtg gag gag ttt aaa cac cct aga gca gcc ttt aaa ttt aag Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys Phe Lys 285 290 295	972
tta atc ttt cag ttc aac ttc taa ttc aaa aat gag ttt att ttt atg Phe Ile Phe Gln Gly Asn Pro Tyr Phe Arg Asn Glu Gly Leu Val Lys 300 305 310	1026

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 Glu Tyr Ala Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro  
 315 321 328  
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 Ile Arg Trp His Arg Gly Gln Asp Arg Gln Ala His Ile His Arg Asn  
 330 335 340 345  
 ggg gaa ggg gaa act att cct ggt ttt ttt aac tgg ttt tta gaa caa 1176  
 Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser Asp His  
 350 355 360  
 agt att cta gaa ttc gaa aga att gca gag att att aac gga gaa ctg 1218  
 Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly Glu Leu  
 365 370 375  
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 Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Met Gly Glu Gly Pro Arg Arg  
 380 385 390  
 gga att cga ggc cca cca agg cag cca gtg gag agc gcc aga tcc ttc 1314  
 Gly Ile Arg Gly Pro Pro Arg Gln Pro Val Glu Ser Ala Arg Ser Phe  
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 caataaaa ttttaagt gagaacac ttgtgatt tttcttca aggtgtga 2329  
 ccacataga acatgacaaa atttgctga gttgtggcat aggaagag atatttctg 2389

atgtgtgtgt atgtgtgtgt atgtgtgtgt atgtgtgtgt atgtgtgtgt 2449  
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atttctctcc ctgctcttaa caaatgaaga agcaggtctg agcttgcatt gtggaagatc 3109  
tccagctctc ttgtagggtg taaggggatg tgtagcatct gtgtggattt tcacggacaa 3169  
gttccagtag gtgggacagt gatgccttca aggttagttt atgacatgt gtgtgtataa 3229  
agaccatcca ccatcaccct tttccctttt ggttttgaag gccttgcctt aagctacctg 3289  
agggtttagg aggtctgaac acacacagtg gagaggttta tctaggtttg gaaactgagt 3349  
aaaagtccag agcaggaatg agcttctgtt gggttgggtt tggaaaagct cacaggaaaag 3409  
aacctgcagg atcaggggtg ggaggggagg cactgaggt gtctctcagg gaagaggggc 3469  
tggggtttaa atagcatgtt tggagggaaga tttctcttca atttttctca agtctctgaa 3529  
ttcaccagta gatttttcta aacaaaatgt aagtcagatg tttctctcaa ttatcttagg 3589  
agtgaacttt atagtgttg agatttaatg gtatagttc ctatgtcac tttttctgag 3649  
taaaatccat ttttttctc tgtttcagc tatgacaaaa ttgatgttta caggtctgtt 3709  
ttttgtttat aattgacaa atgtgcaaaa atacaaaatt ttgttctgtt gcagtatgaa 3769  
gaattcagt atatttcatt aatgtattag cttgttttgc tctctgttca tatatggctc 3829  
tattcttga agataattt gaatgtgato ttccaatgt ctgaatattt taataattat 3889  
agtatctct ttgtgaaaata acctcaaaaa gaaaatag acctgttctt cttctctgat 3949  
atttcttctt ctatgaatgt aattgacatt tatgtctta agcagtttaa gtaagtag 4009  
aattctctct taaaactcaa tgatcattta gttcttctt ctctctctat gtgtttgaa 4069  
gtaatttaa atgatttaa atatttctt gttctctta aaattttaa atattttaa 4129  
aaaaaaaaa aaaaaaa 4148

8212-15

8212-414

8212-PRF

8212-Home regions

8400-55

Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly  
1 5 10 15

Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln  
20 25 30

Cys Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn  
35 40 45

Thr Gly Gly Gly Ser Leu Glu Thr Val Ala Glu Gly Gly Ala Ser Gln  
50 55 60

Asp Pro Val Asp Cys Gly Pro Ala Leu Arg Val Pro Val Ala Gly Ser  
65 70 75 80

Arg Gly Gly Ala Ala Thr Lys Ala Gly Gln Glu Asp Ala Pro Pro Ser  
85 90 95

Thr Lys Gly Leu Glu Ala Ala Ser Ala Ala Glu Ala Ala Asp Ser Ser  
100 105 110

Gln Lys Asn Gly Cys Gln Leu Gly Glu Pro Arg Gly Pro Ala Gly Gln  
115 120 125

Lys Ala Leu Glu Ala Cys Gly Ala Gly Gly Leu Gly Ser Gln Met Ile  
130 135 140

Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser  
145 150 155 160

Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys  
165 170 175

Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu  
180 185 190

Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu  
195 200 205

Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala  
210 215 220

Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met  
225 230 235 240

Gln Arg Arg Ser Ile Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr  
245 250 255

Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp  
260 265 270

Gln Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys  
275 280 285

His Pro Arg Ala Gly Lys Lys Ile Lys Phe Ile Phe Gln Gly Asn Pro  
230 245 300

Tyr Phe Arg Asn Glu Gly Leu Val Lys Phe Tyr Glu Arg Arg Ser Ser  
305 315 320

Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln  
325 330 335

Asp Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro  
340 345 350

Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg  
355 360 365

Ile Ala Glu Ile Ile Lys Gly Glu Leu Trp Pro Asn Pro Leu Gln Tyr  
370 375 380

Tyr Leu Met Gly Glu Gly Pro Arg Arg Gly Ile Arg Gly Pro Pro Arg  
385 390 395 400

Gln Pro Val Glu Ser Ala Arg Ser Phe Arg Phe Gln Ser Gly  
405 410

<10> 56

<11> 2643

<12> DNA

<13> Rattus sp.

<20>

<21> CDS

<22> (1)..(301)

<400> 56

ctg aaa ggg ggg agg ccc agg gtg gtg aac tcc acc tgc agt gac ttc 48  
Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe  
1 5 10 15

aac cat ggc tca gct ctg cac atc gct gcc tgc aat ctg tgc ctg ggc 96  
Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly  
20 25 30

gac gcc aaa tgt tta ctg gag cat ggt gcc aac cca ggg ctg agg aat 144  
Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn  
35 40 45

cga aaa gga cag gta cca gcc gaa gtg atc cca gac cac atg gac atg 192  
Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met  
50 55 60

tcc ctc gac aag tta gag gaa gac ctg ctg gcc aag gaa ttg ctg arg 240  
Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr  
65 70 75 80

ctg cta gaa gac atc gtg cca ctg taa tgc aac ctc cat aaa gtc aca 288  
Leu Leu Glu Gln Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr  
85 90 95





215 57  
 211 267  
 210 387  
 210 341 + 10 51

0400-50  
Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Thr  
1 4 10 14  
Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly  
20 24 30  
Ala Ala Lys Cys Leu Leu Val His Gly Ala Asn Pro Ala Leu Asn Asn  
36 40 46

Arg Lys Gly Gln Val Phe Ala Glu Val Val Pro Asp Pro Met Asp Met  
 5 10 15  
 Ser Leu Asn Lys Ala Gln Ala Ala Leu Val Ala Lys Gln Leu Asn Thr  
 20 25 30  
 Leu Leu Gln Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr  
 35 40 45  
 Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu  
 50 55 60  
 Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly  
 65 70 75  
 Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val  
 80 85 90  
 Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly Ser Val Gly  
 95 100 105 110  
 Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu Phe Ala Ser  
 115 120 125  
 Val Ser Lys Val Ser Lys Ala Val Asp Ala Pro Pro Ser Ser Val Thr  
 130 135 140  
 Ser Thr Pro Arg Thr Pro Arg Met Asp Phe Ser Arg Val Thr Gly Lys  
 145 150 155 160  
 Gly Arg Arg Glu His Lys Gly Lys Lys Lys Ser Pro Ser Ser Pro Ser  
 165 170 175  
 Leu Gly Ser Leu Gln Gln Arg Glu Gly Ala Lys Ala Glu Val Gly Asp  
 180 185 190  
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu  
 195 200 205  
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His  
 210 215 220 225 230 235 240 245 250 255 260 265

&lt;210&gt; 58

&lt;211&gt; 2929

&lt;212&gt; DNA

&lt;213&gt; Rattus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(810)

&lt;400&gt; 58

tat gac tat acc tat aga tgg ggt gag gac ctg aga gaa atc tat ggt 48  
 Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly  
 1 5 10 15

tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta 96  
 Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly  
 20 25 30

acc gga ctg att tat ttc tat aaG gaa gaa agc agc gaa gaa	144
Ala Arg Leu Ala Ser Ile Tyr His And Ala Gly Arg Val Lys Cys Leu	
85 43 45	
gga gag ccc tag aaa gaa ggg ggt ggc gaa gac att gaa gaa gaa gaa	147
Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser	
59 56 60	
cga cat ggt agt gat ttt tet gat cca gaa aca tot gct act ctg ggt	240
Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly	
65 70 75 80	
att gtt cag gtg ttc ttg ggc ttg gat aag aag cta gct cag ggt aag	288
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys	
85 90 95	
cac ttc ccg tcg gtc aac tgg ctc att agg tac agc aag tac atg cgc	336
His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg	
100 105 110	
gcc ctg gac gag tac tat gac aaa cac ttc aca gag ttc gtg cct ctg	384
Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu	
115 120 125	
agg acc aaa gct aag gag att ctg cag gaa gag gag gat ctg gcg gaa	432
Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu	
130 135 140	
atc gtg cag ctc gtg gga aag gcg tct tta gca gag aca gat aaa atc	480
Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile	
145 150 155 160	
acc ctg gag gta gca aaa ctt atc aaa gat gac ttc cta caa caa aat	528
Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn	
165 170 175	
ggg tac act cct tat gac agg ttc tyt cca ttc tat aag acg gtg ggg	576
Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly	
180 185 190	
atg ctg tcc aac atg att tca ttc tat gat atg gcc cgc cgg get gtg	624
Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val	
195 200 205	
gag acc aac gac cag agt gac aat aag atc aca tgg tcc att atc cgt	672
Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg	
210 215 220	
gag cac atg ggg gag att ctc tat aaa ctt tcc tcc atg aaa ttc aag	720
Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys	
225 230 235 240	
gat cca gtg aag gat ggt gag gaa aag atc aag ggt gat tar aca cag	768
Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln	
245 250 255	
tta ctt gaa gat ata gag gaa gaa ttc agt ara ctg gaa gat	816
Leu Leu Thr Asp Met Gln Asn Ala Phe Arg Ser Leu Gln Asp	
260 265	



[illegible]

<210> 59  
<211> 270  
<212> FRT  
<213> Rattus sp.

<400> 59

Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly  
1 5 10 15

Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly  
20 25 30

Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu  
35 40 45

Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser  
50 55 60

Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly  
65 70 75 80

Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys  
85 90 95

His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg  
100 105 110

Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu  
115 120 125

Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu  
130 135 140

Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile  
145 150 155 160

Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn  
165 170 175

Gly Tyr Tar Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly  
180 185 190

Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val  
195 200 205

Ile Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg  
210 215 220

Ala His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Ile Lys  
 225 237 238 240

Asp Arg Val Lys Asp Gly Ala Ala Lys Ile Lys Ala Asp Tyr Ala Gln  
 241 242 243 244 245 246 247 248 249 250

Leu Leu Gln Asp Met Gln Asp Ala Phe Arg Ser Leu Ala Asp  
 251 252 253 254 255 256 257 258 259 260

421 - 67  
 4211 1489  
 4212 120A  
 4213 Rattus sp.

4220 -  
 4221 CDS  
 4222 (1)...(1258)

4400 60

gaa agc cag gag gag gag gat gag gaa cag cag taa cta cta taa 4-  
 Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser  
 1 5 10 15

ggc cat gag cca gga tgg tcc gac cgg gtt cca gtt ccc ggc gtg gcc 96  
 Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala  
 20 25 30

agt aag cgg cag ccg gga ggc ggc aag cca ccc agc cgg gac ggc ctg 144  
 Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu  
 35 40 45

gag tgg ggc ccc tct cca cgc ctt ctt ctc cag ggc ggc agc gag gaa 192  
 Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala  
 50 55 60

ggg ctc cag cgc cag tct gga agc gtt cca cat aca gga agc gcc taa 240  
 Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr  
 65 70 75 80

tta gaa gat gag ccc acc gag att cag gct ccg ggc gga tta ttt gta 288  
 Phe Ala Asp Gln Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val  
 85 90 95

tga ctc tta ctc ctt ggg gtc cgc ttt ccg gcc tgt gcc aac cgg aag 336  
 Ser Phe Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr  
 100 105 110

aca ggc tta cta cct ctt tct ccc cta tca gag cag tcc cgg aag cta 384  
 Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu  
 115 120 125

tgg cca aac ctt cca gct ggc tta tca att agc atg gaa tta att aac 432  
 Trp Phe Thr Pro Pro Ala Gly Phe Ser Ser Arg Met Val Ala Arg Asp  
 130 135 140

gaa tta tta tta gag att tta att tta tta tta tta tta tta tta tta 480  
 Glu Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Phe Arg Arg  
 145 150 155 160

agg gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	625
Arg Pro Gln Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ala Ala Pro	
181 179 175	
gag gat gag gat gag gat gag gat gag gat gag gat gag gat gag gat	676
Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp	
180 181 190	
act caa ttc cgt acc ttc cgt tcc caa tat cat tac cgg cga atc aag	624
Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr	
195 200 205	
cgg acc aga gcc ctg cgc gac gcc tgc gcc ttc tac tgg gga ccg ctg	672
Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu	
210 215 220	
aga gtg cat ggg gcg cac gaa cgg cng cgt gcc gag ecc gtg ggc acc	720
Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr	
225 230 235 240	
ttc ttg ttg cgc gac agt cgc cag cgg aac tgc ttc ttc gcg ctg acc	768
Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe Phe Ala Leu Ser	
245 250 255	
gtg aag atg gct tcg gcc ccg acg agc att cgt gtg cac ttc cag gcc	816
Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala	
260 265 270	
ggc cgc ttc cac ctg gac gcc agc cgc gag acc ttc gac tgc ctg ttc	864
Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr Phe Asp Cys Leu Phe	
275 280 285	
gaa ctg ctg gag cac taq qtg gcg gcg ccg cgc cgc atg ttg ggg gcc	912
Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg Met Leu Gly Ala	
290 295 300	
cca ctg cgc cag cgc cgc ctg cgg ccg ctg cag gag ctg tgt cgc cag	960
Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu Leu Cys Arg Gln	
305 310 315 320	
cgc atc ctg gcc gcc gtg ggt cgt gaa aar ctg gca cgc atc cat ctt	1008
Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu	
325 330 335	
aac ccg gta ctg cgt gac tac ctg agt tcc ttc ccg ttc cag atc	1053
Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile	
340 345 350	
tgaccgggtg gggccgtgcc cgaagatta agtgggagcg actattatt tattattatt	1113
aattattatt atttttcggg aaacacggg gggtctatc cgattajjc ggaggagt	1173
gttgtjjagj rrgatgcc tggacct ct ggaggag attatccg atttgggg	1233
gcctccata ctgtgctcc ctacggjcc ccctgtttgt agcagettgt gctggggc	1293
agagctga cagagjg aggtatatt atttatgt tggagata ttggggg	1353
aggggggg ggagggtat ctggctaat cctctggcg tgagaatat cctatttat	1413

[illegible]

A111 > C1  
 A112 > S01  
 A113 > BR7  
 A113 > Rattus sp.

4400-61  
Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser  
1 5 10 15

Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala  
20 25 30

Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu  
35 40 45

Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala  
50 55 60

Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr  
65 70 75 80

Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val  
85 90 95

Ser Pro Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr  
100 105 110

Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu  
115 120 125

Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn  
130 135 140

Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Pro Arg Arg  
145                   150                   155                   160

Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser Ser Pro Ala Ala Pro  
165 170 175

Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp  
180 185 190

Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr  
195 200 205

Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu  
210 211 243

Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr  
225 230 235 240

The Len Val Arg Asp Ser Arg Glu Arg Asp Cys His His Ala Leu Ser  
241 280

JAN	FEB	MAR	APR	MAY	JUN	JULY	AUG	SEP	OCT	NOV	DEC
<b>TOTALS:</b>						<b>PERCENTAGE:</b>					
269						87%					



Gly Arg Phe His Leu Asp Gly Ser Arg Ala Thr Phe Asp Cys Leu Phe  
275 280 285

Glu Leu Leu Glu His Tyr Val Ala Ala Phe Arg Arg Met Leu Gly Ala  
290 295 300

Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Glu Glu Leu Cys Arg Gln  
305 310 315 320

Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu  
325 330 335

Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile  
340 345 350

<210> 62

<211> 1194

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (130)..(765)

<400> 62

ggcagggctc cggggccggg agcatggcg acagcagccc cggaaccccc agcggggcg 60

ccccgggtcc cggcgccagg gcagccccgg acgatatggc ccacccctcc agctggcccc 120

tggagtagg atg gta gca cgt aac cag gtg gca gcc gac aat gcg atc tcc 171

Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser  
1 5 10

cag gca tca gag ccc cga cgg cgg cca gag cca tcc tgg tcc tgg tct 219

Pro Ala Ser Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser  
15 20 25 30

tgg tcc tgg cag gcg gcc ccg gcg cgt ccc cgg ccc tgc cag gtg gtc 267

Ser Ser Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val  
35 40 45

cag gcc cag gat ccg gcc gac aat cag ttc cgc acc ttc cgc tcc cag 315

Pro Ala Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His  
50 55 60

tct gat tac cag cgc atc acg cgg acc agc ggt ctc atg gac gcc tgc 363

Ser Asp Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys  
65 70 75

gac ttc tac tgg gga ccc atg agc ggc cat ggc ggc cag gaa cgg ctc 411

Gly Phe Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu  
80 85 90

cgt gcc gag acc atg gcc acc ttc atg gtc cgc gac att cgt cag cgc 469

Arg Ala Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg  
95 100 105 110

[illegible]

Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Ile  
 65 70 75 80

Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala  
 85 90 95 100

Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Glu Arg Asn Cys  
 105 110 115 120

Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg  
 115 120 125

Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr  
 130 135 140

Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg  
 145 150 155 160

Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln  
 165 170 175

Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu  
 180 185 190

Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe  
 195 200 205

Pro Phe Gln Ile  
 210

<210> 64

<211> 600

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (52)..(336)

<400> 64

cttcacaaaga ctgcagcgcg ttagggccca ggttccaaca gattcttcaa a atg caa 57  
 Met Pro  
 1

tcc caa atg gag cat gcc atg gaa acc atg atg att aca ttt tgc agg 105  
 Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe His Arg  
 5 10 15

ttt gca ggt gaa aaa aac tac atg aca aag gag gac ctg aga atg ctt 153  
 Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu  
 20 25 30

atg gaa agt ggt ttc cat ggt ttt ttt gaa aat caa aag ttc gtt ttt 201  
 Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp Pro Leu  
 35 40 45 50

Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly

1	5	10	15	20
gtt ggt aat tta tga tta tta tta tta tta tta tta tta tta tta	25	30	35	40
Val Gly Lys Phe Cys Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu				
atg ggt gat gac ctc aca att ggt gta gag ttt ggt ggt ggt ggt ggt	45	50	55	60
Pro Val His Asp Leu Thr Ile Gly Val Gln Phe Gly Ala Arg Met Ile				
acc att gat ggt aaa cag ata aaa ctc cag atc tgg gat aca gta ggt	65	70	75	80
Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly				
cag gag tcc ttt cgt tct atc aca agg tca tat tac aga ggt gca ggt	85	90	95	100
Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala				
ggg ggt tta cta gtg tat gat att aca agg aga gac acg ttc aac cac	105	110	115	120
Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His				
ttg aca acc tgg tta gaa gac gcc cgt cag cat tcc aat tcc aac atg	125	130	135	140
Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met				
gtc atc atg ctt att gga aat aaa agt gac tta gaa tct agg aga gaa	145	150	155	160
Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu				
gtg aaa aag gaa gaa ggt gaa gct ttt gca cga gag cat gga ctt atc	165	170	175	180
Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile				
ttc atg gaa act tct gcc aag act gct tct aat gta gag gag gca ttt	185	190	195	200
Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe				
att aac aca gca aaa gaa att tat gaa aaa atc caa gaa ggt gtc ttt	205	210	215	220
Ile Asn Thr Ala Lys Glu Ile Tyr Gln Lys Ile Gln Glu Gly Val Phe				
gac att aat aat gag gca aac ggc atc aaa att ggc cct cag cat gct	225	230	235	240
Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala				
gct acc aat gaa tct cac gga ggc aac caa gga ggt cag cag gaa ggt	245	250	255	260
Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly				
tta tta tga tta tga	265	270	275	280
Gly Gly Cys Cys				

&lt;210&gt; 6"

&lt;211&gt; 212

&lt;212&gt; FRT

&lt;213&gt; Rattus sp.

&lt;420&gt; 67

Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly  
1 2 3 4 5 6 7 8 9 10 11 12Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln  
13 14 15 16 17 18 19 20 21 22 23 24 25Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile  
26 27 28 29 30 31 32 33 34 35 36 37 38Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Thr Asp Thr Ala Gly  
39 40 41 42 43 44 45 46 47 48 49 50Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala  
51 52 53 54 55 56 57 58 59 60 61 62 63Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His  
64 65 66 67 68 69 70 71 72 73 74 75 76Leu Thr Thr Thr Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met  
77 78 79 80 81 82 83 84 85 86 87 88 89Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu  
90 91 92 93 94 95 96 97 98 99 100 101 102Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile  
103 104 105 106 107 108 109 110 111 112 113 114Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe  
115 116 117 118 119 120 121 122 123 124 125 126 127Ile Asn Thr Ala Lys Glu Ile Tyr Glu Lys Ile Gln Glu Gly Val Phe  
128 129 130 131 132 133 134 135 136 137 138 139 140Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala  
141 142 143 144 145 146 147 148 149 150 151 152 153Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly  
154 155 156 157 158 159 160 161 162 163 164 165 166Gly Gly Cys Cys  
167 168 169 170

&lt;210&gt; 68

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Rattus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(13)

&lt;4400&gt; 68

Met Val Leu Leu Lys Gln Tyr Arg Val Ile Leu Pro Val Ser Val Asp  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 42

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 144 Met Arg Val Lys Asp Pro Val Lys Gly Met Thr Ala Asp Asp  
 267 268 270

<210> 69

<211> 2283

<212> DNA

<213> Simian sp.

<400> 69

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 catgaacttg gaagggttg aaatgataga agttctgata gtcattgtgc tttttgttaa 180  
 attattggaa cagtttgggc tgattgaaga aggtttagaa gacagcgtgg aagatgaaat 240  
 ggagatggcc actgtcaggc atcggcctga ggccttgag cttctggaag cccagagcaa 300  
 attaccaag aaagagcttc agatccttta ccagaggattt aagaacgaat gccccagtgg 360  
 tgttgttaat gaagaaacct tcaaagagat ttactgcag ttctttccac agggagaact 420  
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